

A - caGWAS Glossary

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Acronyms, objects, tools and other terms referred to in this online help are described in this glossary.

| Term | Definition |
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| Allele | Any one of a number of viable DNA codings occupying a given locus (position) on a chromosome |
| caGWAS | Cancer Genome-Wide Association Study |
| case-control study | A study including subjects who already have a condition, and those who don't have the condition, to determine if there are characteristics of the affected subjects that differ from the unaffected subjects |
| CBIIT | Center for Biomedical Informatics and Information Technology |
| CGEMS | Cancer Genetic Markers of Susceptibility |
| Completion rate | For a set of genotype data (either by SNP or for a single individual), the percentage of genotypes completed successful compared to genotypes attempted |
| confidence interval (CI) | A range around a measurement that conveys how precise the measurement is |
| dbSNP identifier | The identifier for a cluster of polymorphisms in dbSNP, NCBI's central repository for single base nucleotide substitutions (SNPs) and short deletion and insertion polymorphisms (aka "rs number") - see http://www.ncbi.nlm.nih.gov/SNP |
| Genome | The complete sequence of DNA contained in an organism or a cell, including both the chromosomes within the nucleus and the DNA in mitochondria |
| Genome-wide association study (GWAS) | An approach that involves rapidly scanning markers across a person's genome to find SNPs associated with a particular condition |
| Genomic location | The physical location of a feature (e.g. gene, exon, SNP) on a genome or chromosome |
| Genotype | The genetic makeup encoded in an individual's DNA. When related to SNPs, the genotype refers to the nucleotides at the SNP locus on the two DNA strands of the sample. |
| Hardy Weinberg p-value | The Hardy-Weinberg principle (HWP) states that, under certain conditions, after one generation of random mating, the genotype frequencies at a single gene locus will become fixed at a particular equilibrium value. It also specifies that those equilibrium frequencies can be represented as a simple function of the allele frequencies at that locus. |
| HUGO gene symbol | A gene symbol approved by and included in the HGNC http://www.gene.ucl.ac.uk/nomenclature |
| Minor allele frequency | The frequency of chromosomes in the population carrying the less common variant of SNP |
| NCBINCBI | National Center for Biotechnology Information, see http://www.ncbi.nlm.nih.gov |
| Odds ratio | <p>The ratio of the odds of an event occurring in one group to the odds of it occurring in another group, or to a sample-based estimate of that ratio.</p> <p>An odds ratio of 1 indicates that the condition or event under study is equally likely in both groups. An odds ratio greater than 1 indicates that the condition or event is more likely in the first group. And an odds ratio less than 1 indicates that the condition or event is less likely in the first group.</p> <p>The odds ratio must be greater than or equal to zero. As the odds of the first group approaches zero, the odds ratio approaches zero. As the odds of the second group approaches zero, the odds ratio approaches positive infinity.</p> |
| P-value | In the case of SNP disease association studies, a statistical measure of evidence that the SNP is associated with the disease phenotype |
| SNP | Single nucleotide polymorphism: A SNP occurs when corresponding sequences of DNA from different individuals differ at one DNA base; for example, where the sequence AAGCCTA changes to AAGCTTA. |

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| Panel | A collection of SNP loci genotyped together on a genotyping platform (e.g. Illumina) |
| Whole genome rank | The rank of significance (disease phenotype association) of the specific SNP in the analysis (the lower the rank, the higher the significance) |